Figure 1.

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: new_S100_cytokine
Sequence 2: G491246
                                   110 aa
Sequence 3: W27152
                                    98 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 23
Sequences (1:3) Aligned. Score: 34
Sequences (2:3) Aligned. Score: 29
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1:
                            Delayed
                            Delayed
Group 2:
Sequence: 1
              Score: 0
Sequence: 3
              Score:839
Sequence: 2
              Score:724
Alignment Score 444
CLUSTAL-Alignment file created [/data4/genetools/lrastelli4630clustalw]
```

Multiple Alignment:

Probe Size: 104 Amino Acids Probe File: Irastelliblocks.seq Target File (s): blocks.dat Records Searched: 4034

Scores Done: 4034
Alignments Done: 535470

Mouse-over to show defline and score. Click to show alignments

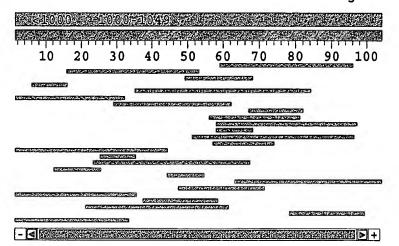


Fig. 4A

Replacement Sheet Application No. 10/614,599 5/9

| | | | | | ט וכ | | | | | | | | | | | | | |
|--|--|--|---|-------------------------------|---|---|---|---|---|---|-----------------------------------|---|--|---|---|--|---|---|
| AA# 59 SNCGLEEKi aNLGSCADSXLeFRSFWelIGeAAKSVK (SEQ ID NO:12) 16 DVERAIETLIKAFHQYSVEGGKETltpsElrdLvtQQ (SEQ ID NO:13) 49 VTQQIphlmpSncgleEKi (SEQ ID NO:14) | o ridenakters (SEZ ID NO.12) 35 GCAELITPSELRDIVTQQIphinpsncgleEkiANIgscndSkleFRsf (SEZ ID NO.16) 0 mgCcRSAnAedAOefSdVERaIEtlIKNFhgY (SEQ ID NO.17) | 29 hqYSvegGKetltPselrdLvTQQlPHlMpsnC(SEQ_ID NO:18) 67 janlgSCNdsKlEFR (SEQ_ID NO:19) | 56 IMpsNcgleEkiAnicScndsklef (SBQ ID NO:20) | 58 PSNCGLEBKI (SEQ ID NO:22) | 51 gqlpKlmpsnCgleEKIanlgScndsKlefRsfWeligeaaksvk (SBQ ID NO:23) | 57 mPSnCgleEKIanlGsC (SEQ ID NO:24) | -1 mggCrSaNAEDaQeFsDVeRaIeTlIknfhQySveggketLIpSE (SBQ ID NO:25) | 25 ikNFhqYsVE (SEQ ID NO:26) | 23 TLIknfhqySveggkeTlTPSElrdlvtQQlphIMPsNcGLeeK(SEQ ID NO:27) | 12 qefSDVERAIETL (SEQ ID NO:28) | 44 ELRDIA/TQQL (SEQ ID NO:29) | 63 LeekiaNIgScnDsKlEfrsFwelIgBaaKsVKlERpvRgh (SBQ ID NO:30) | 47 dLVTggLPhIMpsncGlEekIANL (SEQ ID NO:31) | 1 qQCRsANaedaqEFsDVerAIET11knfHqYSvE (SEQ ID NO:32) | 37 keTLTpseLrdlVtQQlpKln (SEQ ID NO:33) | 21 IeTlikNfhqysveGGKETLtpselrdlvTQQlphlMpGN (SEQ ID NO:34) | 78 LEFRSFWELIGEAAKSVKLER (SEQ ID NO:35) | -2 MggcrsAnAedAgEfSdverAiEtliKNfhqySvE (SEQ ID NO:36) |
| RF 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | - 0 0 | 0 0 | 0 0 | 0 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 / | 0 / | 0 1 | 0 | 0 | 0 | 0 | 0 |
| Score 1057 1038 1021 | 990 989 | 987 | 976 | 9/6 | 974 | 974 | 973 | 972 | 970 | 968 | 967 | 296 | 964 | 963 | 963 | 960 | 960 | 960 |
| Strength Score RF AA# 1336 1057 0 59 1345 1038 0 16 F 1456 1021 0 49 | 1758 1758 1412 | 1539 | | 990 | C | 1433 | 1508 | 1127 | 1692 | 1298 | 1092 | 1826 | 1552 | 1528 | 1567 | 1580 | 1200 | 1908 |
| Description 0 3-100/ICaBP type calcium binding protein. 0 3-100/ICaBP type calcium binding protein. 0 Bacterial type II secretion system protein F | 0 Bacterial themotaxis sensory transducers prot 0 Phosphoenolpyruvate carboxykinase (ATP) prote | <pre>0 Prokaryotic-type carbonic anhydrases proteins 0 Ergosterol biosynthesis ERG4/ERG24 family pro</pre> | 0 Lysosome-associated membrane glycoproteins du | O PH domain proteins profile. | 0 Hyotoxins proteins. | O Phosphatidylinositol-specific phospholipase X | 0 Glypicans proteins. | 0 Membrane attack complex components / perforin | O Urease nickel ligands proteins. | O Phosphoglycerate mutase family phosphohistidi | 0 Ribosomal protein L23 proteins. | 0 2'-5'-oligoadenylate synthetases proteins. | O Formate and nitrite transporters proteins. | 0 Glycoprotein hormones beta chain proteins. | O Vinculin family talin-binding region proteins | 0 Beta-lactamases class B proteins. | 0 Heat shock hsp20 proteins family profile. | 0 Hydroxymethylglutaryl-coensyme A lyase protei |
| AC# BL00303B BL00874A BL00874A | BL005321 | BL00704A BL01017E | BL00310E | BL50003 | BL00459 | BL50007C | BL01207B | BL00279B | $\overline{\text{BL01120D}}$ | BL00175B | BL00579A | BL00832B | BL01005C | BL00261A | BL00663A | BL00743A | BL01031B | BL01062C |

Fig. 4A (Continued)

Figure 4B

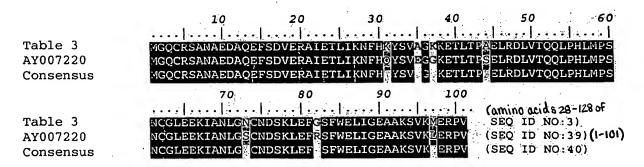


Figure 4C

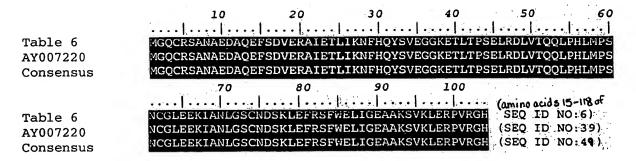


Figure 4D

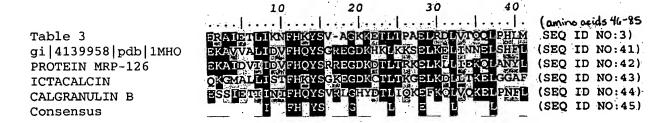


Figure 4E

20 30 40 (amino acrds 33-72 Table 6 SEQ ID NO:6) gi | 4139958 | pdb | 1MHO (SEQ ID NO:41) (SEQ ID NO:42) PROTEIN MRP-126 ETIIMEFHQYS<mark>V</mark>RESHYDTLIOKEFROLV TTIIDEFHQYSRRESHPDTLSKKEFROM (SEQ ID NO:44) CALGRANULIN B (SEQ ID NO:46) CALGRANULIN B (SEQ ID NO:47) Consensus

| | ************************************** |
|-----------|--|
| | • |
| 65677221+ | GAATTCCAGAGGGAGTTCTCAGTGCCCCCGGACAGGCCTCTCCAGCTTCACACTCTTGGC |
| AA315020- | TGCCCCCGGACAGTCCTCTCACACTCTTGGC |
| consensus | GAATTCCAGAGGGAGTTCTCAGTGCCCCCGGACAGGCCTCTCCAGCTTCACACTCTTGGC |
| | |
| 65677221+ | CGCTTCTCCAATCAGCTCCCAGAAACTCCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC |
| AA315020- | CGCTTCTCCAATCAGCTCCCAGAAACTCCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC |
| consensus | CGCTTCTCCAATCAGCTCCCAGAAACTCCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC |
| | |
| 65677221+ | CAGGTTGGCAATTTTCTCTTCCAGGCCACAGTTGCTCGGCATGAGATGGGGCCAGCTGCTG |
| AA315020- | CAGGTTGGCAATTTTCTCTTCCAGGCCANAGTTGCTCGGCATGAGATGGGGCAGCTGCTG |
| consensus | CAGGTTGGCAATTTTCTCTTCCAGGCCACAGTTGCTCGGCATGAGATGGGGCAGCTGCTG |
| | |
| 65677221+ | GGTGACCAGGTCCCGTAGCTCAGAAGGGGTCAGCGTCTCCTTCCCACCCTCCACGGAGTA |
| AA315020- | GGTGACCAGGTCCCGTAGCTCAGAAGGGGTCAGCGTCTCCCTTCCCACCCTCCACGGAGTA |
| consensus | GGTGACCAGGTCCCGTAGCTCAGAAGGGGTCAGCGTCTCCTTCCCACCCTCCACGGAGTA |
| | |
| 65677221+ | CTGGTGAAAGTTCTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTC (SEQ ID NO: 37) |
| AA315020- | CTGGTGAAAGTTCTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTCCTGAGC |
| consensus | CTGGTGAAAGTTCTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTCCTGAGC |
| | |
| AA315020- | ATCCTCTGCGTTGGCTGACCGACACTGTCCCATGGTGCTCACTGTGTCTGGTCCTTTTGGT |
| consensus | ATCCTCTGCGTTGGCTGACCGACACTGTCCCATGGTGCTCACTGTGTCTTGGTCCTTTGGT |
| | |
| AA315020- | GAGAGTTCTGTTGTCCTAT (SEQ ID NO: 48) |
| consensus | GAGAGTTCTGTTGTCCTAT (SEQ ID NO: 5) |
| | |